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By (Daniel Miranda)



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Lemieux et al.

Application No.: Unassigned

Filed: January 9, 2002

For: BRASSICA POLYMORPHISMS

Examiner: E. Campbell

Art Unit: 1656

PRELIMINARY AMENDMENT UNDER
37 C.F.R. § 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

In order to comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, Applicants enclose a paper copy of the Sequence Listing filed in Application No. 08/813,507, filed March 7, 1997. In accordance with 37 C.F.R. § 1.821(e), please use the computer-readable form filed in Application No. 08/813,507 as the computer-readable form for the instant application. The information in the paper copy of the Substitute Sequence Listing enclosed herewith is identical to that which is in the computer readable form, as required under 37 C.F.R. § 1.821(f). It is understood that the Patent and Trademark Office will make the necessary changes in application number and filing date for the computer-readable form that will be used for the instant application.

Please replace the paragraph beginning on page 4, line 9, with the following:

Fig. 1 shows probe array tiles (SEQ ID NOS:3-29) for two allelic forms of the Brassica 18A2 polymorphism (SEQ ID NOS:1 and 2).

Please replace Table 1, beginning on page 8, line 10, with the following:

Marker Name	Sequence	SEQ ID NO
1-85/5B5/86-1	AGCAAGCTTACATGGCTGGA [G/T/AA] GAGAGTCCTCGAGATCAACC	30
2-85/5B12/N3-1	CCTTGATCTCTCAAAGTAATC [A/G] TCTCACCGGAAGATCCCTGA	31
3-85/5C3/86-2	ACCATCCATTAAACTGTATC [A/G] TCGCAATCTAACCAAAAGTT	32
4-85/5E1/86-1	TAAGCAAAGAGAGTCTTAC [C/A] GTCTGCTGCATGATAACCC	33
5-85/5E1/86-2	CTACTGATACTGTAAACCCACCC [A/C] ATCCCCAAATTAAAGCAA	34
6-85/6A11/86	ATCCTATTGGTAGTAAACACA [G/A] ATTGAGTTAATGTTGCAGGG	35
7-N1/6A11/N2	AGGCAAAGGGTAGTTGCAA [G/A] ACTGCTTCTCACGGAGGTAAT	36
8-N1/6A9/N2-1	CCAGCTTCAATGTCATGCATG [C/A] TTGTTGTCGATGCCAAAGTC	37
9-N1/6A9/N2-2	AAAGTTCAATTACGATGATCT [A/G] ACCCTGCAGTCATCCATGGAA	38
10-85/6A12/86	CTTCCCCCCTCAATAACCTC [T/G] TTCAAAAGTGAAGTGCAG	39
11-N1/6D1/N2-1	ATTTTGTTTGTCTTGTCTG [G/C] GGTCAAGGTCAAGAACAAAGTT	40
12-N1/6H5/N2	AAACCAAGGCCACCTCCCTTA [C/] CCACCTCATCGTTTCCTTTC	41
13-86/6F11/N2-2	GATTTCGACCCGAGTCTCAC [G/T] GAGGTGAGTTATCGCTTT	42
14-N1/6F11/N2	TAGGACAGGCCAAACAAATCTA [C/A] GGGTCAAAATCCGATTTCG	43
16-N1/8B5/N2	ACTCAAAAAAACGATAACCTC [G/C] GCCGTCTCGCCGTCTCCGC	44
17-N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC [T/A] CAGAGTCGCAAGGATCTCGAA	45
18-85/8D4/86-2	CTGATCTTGAAGGGAGACCA [A/G] CCACAAGGTCCATCCTATG	46
19-85/8H11/86	AGTGCAGGGCTCAGTTGGAT [G/T] ATTAGGGTGTCAAGTAATCA	47
20-85/10B8/86	NAGGTCCATGATGATGACAA [T/A] AAAGGTATTCCACATGTCAA	48
21-N2/10B8/N3-2	ACATCCAACTTTCTCCAGT [T/C] CTTTATTCTATCCCTGATTG	49
21-N2/10B8/N3-2	ACATCCAACTTTCTCCAGT [T/C] CTTTATTCTATCCCTGATTG	50
22-N2/10B8/N3-1	AAGGTATTCCATGGTATAC [A/C] TCCAAACTTTCTCCAGTTCT	51

23 - 85 / 10B9 / 86	GACCTCTTGGAAAAGAAAAAG [T / C] TGTAACCGCGTTCGAGATTCG	52
24 - 10C8 / N2	ATAGAAACCGCCGATGCTCA [A] GGACACGCCACCGTCTTCGT	53
25 - 10C8 / N2	CACTTCTTCGTTGGCTAAAT [T] CTTGGCCAGCCGGTCTCA	54
26 - 10D2 / N1	GTTATCATCAGTACCGGTAT [T] AACCCCAAGGCTAATTCTTA	55
27 - 85 / 10D2	TGGGTATCTACGGACTGAT [C] ATCGCTGTTATCATCAGTAC	56
28 - N1 / 10E12 / N2 - 1	GGAAATTCAAACTCGCCAAAC [G / T] TCTTCATTGCTGTCGTCGGC	57
29 - N1 / 10E12 / N2 - 2	TCCCTAACGGCTTCAAGCGCA [C / G] CGGCTGGCTCATGGGTGTCC	58
30 - N1 / 10F4 / N2	TGTATCTATGCGGTGGCTGC [G / C] GTCTCCGTTCGGCCAGTAC	59
31 - 10F4 / N2	GGCCCAAGTACCCGCCGGTTAC [A] ATCTCAGTCCCTCACGTCC	60
32 - 85 / 10F4 / N2	GGCCCAAGTACCGCCGGTTAC [G / A] ATCTTAATGCGCTTCACGTT	61
33 - 85 / 10F9 / N1 - 2	AACTTGGAAATTCCACAACTT [G / C] AGAAACCTTCGATGGTGCC	62
34 - 85 / 10F9 / 86	CGGTACTGGAAAGCTGGAG [C / G] ATCAAACTTGGAATTCCACAA	63
35 - 86 / 10F12	AAAAGTGCCTATTGTTCAGGT [G] GATGCTGCTCCGGTCAAGCA	64
36 - 85 / 10H6 / 86	GTCAAAAGGCCACGGATTCAA [G / A] AACGTGCTCTTGGCCCT	65
38 - 85 / 10F12 / 86	AAACCAGGGTCCATTGATGTTG [T /] GTCTACAAAGCTTCCAACAA	66
39 - 85 / 11B7 / 86	AAANACCTGAGCTCATGCTT [C / T] TGACCCCATGTTCTTGGCACC	67
40 - 85 / 11C4 / 86	TTTGGGACCGTTGGAGTTGC [A / G] TCTGGGGCTATGACGGTGGA	68
41 - 85 / 11D4 / 86 - 2	AATCTTTGCCATTGCTGTCA [A / G] TATCTTGTCAAGCTTCAGCT	69
43 - N2 / 11D11 / N3	GACAACGGCTGGTGGTATTGC [C / T] GAAATGGCTGGAATGAGCCA	70
44 - 86 / 11D11 / N3	GCTGCTCTAGGGATGCTCAG [C / T] ACCATGCCACCGGTTGGC	71
45 - 85 / 11D11 / 86	ATGCTCAGGACCATGCCAC [T / C] GGTTTGGCGATTGATGCTTA	72
46 - N2 / 11E3 / N8a	GAGAAAAGTGCCTGGAGAT [C / T] TACAAaGTCACACTGATGGC	73
47 - 86 / 11E3 / N2a	AAATGCTTGTGGAGATTACA [G / A] GTCCCATACTGATGGCGAGG	74

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48-86/11E3/N2b	AATGCTTGGAGATcTACA [G/A] GTCCATACTGATGGGCAGG	75
49-85/11F12/86	AATGATTTGGTTGAGGAAGCA [T/A] ACAGCTGGTACGGTTGATAT	76
50-85/11F7/86	GATAGGGCGAAGAGAGGGAA [G/A] AGTCCCTGAGAGGAAAGAGAT	77
51-85/11H2/86-2	CTCTCTCTCCACAAAGACAC [A/C] GCTTTCTCCATGACCTTCGG	78
52-85/11H5/86-2	TCTCTGACGCTCATGAAAGCT [C/A] ATGGCAAAATTGCTGATGGA	79
53-85/11H6/86-1a	GTATCGATCGGTGGTCCG [T/C] GAAACCCAAAATCACCTTT	80
54-85/11H6/86-1b	GTATCGATCGGTGGTCCG [T/C] GAAACCCAAAATCACCTTT	81
55-85/12B6/N3	CGTCAGGCCCTTCGCGCG [A/C] GTCTGCCCTCCGCAACCGTGC	82
56-86/12B6/85a	TGTCTTCCGTCAGCCTTC [C/T] TCCGCCAGTGGTCCCTCCG	83
57-86/12B6/85b	TGTCTTCCGTCAGCCTTC [C/T] TCCGCCAGTGGTCCCTCCG	84
58-86/12B11/85	TCAGGGTTAACCTCTATATAT [T/] ATATTTCATGGTATGAAGGT	85
59-n1/12B11/N2-2	TATCCTGCAAATGACATT [T/C] CCTTCAGGTTCTAGAACGCTG	86
60-85/12C2/86	CGAGAACAGAACAGAACAGAGA [C/] TGGAACACCGTGGACAGTAC	87
62-12C11/N2	ACGGGTCCCTAGGCCATGGC [T] ATTTCCTCACCGTTCTGG	88
63-N1/12D10	TTGGGCTTTCGGTGGTATGA [T] CTTCTGCCCTCGTCTATTGCA	89
65-85/12F4/86-1	TCCCTTGATTCCTTAATAATC [A/T] TTGGCTGGGGTCTTCTAA	90
66-12G5/N1	GCTTGAATAACGATGTCAC [T] CTGCCTCGCGTACGGCGGA	91
67-85/12G8	CTAAAAAGATCGACGAGTGT [C] CCTTAACGCTCCATCTAT	92
68-12G9/N1-1	AGGTGGGTTAGCGTGGCAT [C] CGATCCATTGGATGGATCCA	93
69-85/12G9/	NGTGGGTTACCGTATCATT [T] GATCCATTGCAATGGATCGAG	94
70-12B11/N2-1	GCGGATCCATTGGGTCT [T] GATGGATTGGTTCTATCCCG	95

71 - /12B11/N2 - 2	TATCCTGCAAATTGACATT [C] CCTTCAGGTTCTAGAAGCTG	96
72 - N1/12E10	TACCA CGGT CGTACTGGTCG [A] TGTCTGGAACGTCACCAAGC	97
73 - N1/13A3/N2a	CTGTCTCAGTTGTGGATC [C/G] AAATCGAATCGAAAGCGTAC	98
74 - N1/13A3/N2b	CTGTCTCAGTTGTGGATC [C/G] AAATCAAAATCGAAAGCGTAC	99
75 - 13E8/N2	ACACTGTTGGAGGACGTGAA [G] AAGATATTCAAGACAAACATC	100
76 - N1/13F6/N2 - 2	TCTTTTGGTATCTTGTTGAGT [C/T] GTTACGGCCTGTCAAACACCCG	101
77 - 13F8/N2 - 1	GGAAACCTTAGGGAGCCACA [G] CTCCTTATGCTTAAGGGCGT	102
78 - 13F8/N2	GATCATAGTATCCGGCGGAA [C] CCTAGGGAGCCCACAGCTCC	103
79 - 85/14B5/86	TTCGGGGGGTCAATCCGGGC [A/G] GAAGACATTGTCAGGTGANN	104
80 - N1/14C2/N2	GCACCAACATTGTAAACCTA [T/G] AGCTTCTCTCAGGCCACCT	105
81 - 85/14C2/86 - 1	GCTGCCACATAGTGAACCTA [T/A] AGCTTCTCTCAGGCCACCT	106
82 - N2/14C2/85 - 2	GCACCAACATTGTGAACCTA [G/A] AGCTTCTCTCAGGCCACCT	107
83 - 85/14C2/86 - 2	AGTACATAGCTATTGACTAA [C/G] TTAAGTTCTTGTATTGTTG	108
84 - N2/14C2/85 - 1	CCTCTATCGCCATGGTTGC [A/T] CCAACATTTGTGAAACCTAGAG	109
85 - 85/14E2/86 - 2	TTGACCCCTGGCAAGGCCACC [G/T] GTCAAGCCATGCTGCAGCCT	110
86 - 85/14E2/86 - 1	AGGCTGCCCTCTCCCAATT [A/C] AAAGCCAACCTCTAAACCAA	111
87 - 85/14E8/86	AAACATGGAAAGGCCCTGATA [/G] TCACCGTCAAGCTCACCGTC	112
88 - 85/14E12/86	CAACCTGAAAAATTGTTTA [C/A] CAACGGCCCCGTTCTCCA	113
89 - 14H10/86	AAGGCCAACAAACGACATTAC [C] TCCATCGTTAGCAACGGAGG	114
90 - 85/14H10/86	TCACCGGGCTTGAAGTCTTCC [G/T] CTGCATTCCCAGTCACCCGC	115
91 - 85/15A6/86	ACTCAGCTTTCTTATGCCCTC [G/] ACTTGGCAGACACCGAATCCA	116

92-85/15C4/86	TGGGGCTAACATCTGGTG [G/T] TCACCTTAACCCAGCCGTAN	117
93-85/15E5/86-1	CGAGGATCACTTCTCTCTGT [G/T] CAAGAAGAACGTCGGCAAGG	118
94-N1/15E5/N2-1	CTGTTCAAGAACGAAAGTTCGG [C/T] AAGGTCTACGCTTCCCGGA	119
95-N1/15E5/N2-2	CCCTCTGCTCGTCAGGGCGT [T/A] ACGCAGTTCTCGGATCTGAC	120
96-86/15E5/N2	CCCGCGAGGAGGACGACTAC [A/T] GATTCTCCGTTTCAAATCC	121
97-15E9/86	TCCACTCGCCGGAAAGAAC [T] CGAACAAACCGTTGTCTACTT	122
98-N2/15E9	ATGGCTCGCGACGGGTCTCC [G] GTAAACCTCGGAGAGGAGAT	123
99-N2/15E9/86	GCCGACTCTCGAACGTTCTT [A/] ACTCCACTCGCCGGAAAGAAC	124
100-85/15E9/86-1	GAATCTAGGAGAGCAGATCT [T/G] CCTCTCTATCTCAATGTTC	125
101-85/15E9/86-2	TCCACTCGCCGGAAAGAAC [C/T] CGACAAACCGTTGTCTACAT	126
102-N1/15E9/N2-1	GTCAATGAGATATTCACTAC [A/G] CGGACTCTCGAAGCTTCTTA	127
103-85/15F1/86	GCAGGTAAAATTCTACAGAC [C/A] TCCCTTTCAATTGTAGTTA	128
105-85/15F10/86	GTGCCCTAAAGATAACCCCTCA [A/G] GCTTGGTGTCTGGCTAATG	129
106-N2/15G1	TTCCTCCACAGGTGAAACT [T] GCTAACATTCTTCCAAAGTA	130
107-N1/15H7/N2	TATGTATCAGGACAAATGTTG [GA/TT] GTGACTGTGGTTGCATCCAT	131
108-N1/16A1/N2-1	GCTAAGCTAACGCAACTGCCA [C/T] CAATCAGGGCAAGCTAAAGG	132
109-85/16A5/86	TATACACTCTTAAAGCGT [G/C] TGTGTGTACCCATCTCTCT	133
110-N1/16B6/N2	ATGGCTGCGTATTGGCTGTC [C/T] AAGGCTGGATCTGGTCCCCA	134
111-85/16B6/N1	GGATCCCATCTCAACTATGGT [A/C] GTATTATCGTTGAGGCTAGG	135
112-85/16B7/86	GTATGTGATTCCGAAGAGAA [T/] CAAACTAACGTCGGAGAAAG	136
113-N1/16D6/N2	GCTAAGGTAGTTGGAGGAGC [CAA/GTG] CCACAGGCCACGGGACTAAAGG	137
114-85/16D10/86	CTCAACGTTAGCAAGTAATAA [T/G] ATACTGTCTTATTATGGTTA	138

Page	Sequence	Description	Page
115-N1/16E9/N2	AGACTTCCCCATTCTCTTC [T/A] CCATCCACCGTCGAAACCCA		139
116-85/16H3 / 86-1	ACTTCGAAACTGTAAACCTA [A/T] ACTTTAAGAGTTAGAGCTA		140
117-85/16H3 / 86-2	CACCATCGGAGAAAGAGGT A [C/T] TTCGAAACTGTAAACCTAA		141
118-85/17A5 / 86	CTAAGGGGTCTCTGAAGAA [A/G] TACAGAGAGTCGAAGAGAT		142
119-85/17C7 / 86	CCGGGGACGAGCCTTCTTC [C/A] TCTGCTCCACCCGGAGCGCC		143
120-85/17F7 / 86	GAGGAGTAGTCTCCATGGCC [G/] AAGAACAGCGTGGAGACCTG		144
121-85/17G12 / 86	GAAAGTTAGGGCTTCTTAAGAT [C/T] AAGTTGGCAAGGGCTTAAAC		145
122-85/18A2 / 86	TCAAAACTAATATTCTTT [G/C] TTGATTGTAATAAACAGGT		146
123-85/18A11 / 86	TTCCAGTGAAGGCATTGT [T/G] CTCCMAAAATCTCGCTCTGCG		147
124-85/18F5 / 86	AAGCAGCTCTGACTTGAATG [C/A] GAGAGGTTAATCAGACTGTG		148
125-85/18H10 / 86-3	TAGATTGAAGCAATCAAGAA [G/A] ATCTCAGACTTCATCACCCA		149
126-85/19B3 / 86	GCATCCAACTCCAAGGTGA [C/C] CCTGCCAAGGTGCTGCTAACT		150
127-85/19C8 / 86	GAGCTCAGGGATGGGGATC [A/T] GACTACCTTGGAAAGGGTGT		151
128-N1/19F4 / N2	TGGGGTTAGTCGAAATAGGT [A/T] AAATGCTTTGAGTATGTGTA		152
129-N1/19H1 / N2	TACGGCGAGGCACGGACTTGC [G/A] ACGCAAGCAATCGAGCTTT		153
130-85/20B4 / 86-1	GAAAGCCCATTGGTACGGAGCG [G/A] GAGAGGTTCAAGTACTTGGG		154
131-N1/20B12 / N2	AACGGGGTCACTGCTAAATCA [T/A] AAGGATCACAAAGGCTGGAC		155
132-85/20C12 / 86	CTAGCCTACTTTGGAAAAAG [T/T] TTGCTTATGTGTTGTTG		156
133-85/20D2 / 86	GACTTCAAGGACTTGCCTAAATCA [A/C] AAATGCTCCGACGGCTGTCAA		157
134-85/20D3 / 86-2	GAGGAGGGCTACATGGCAGGT [G/A] AAGAGGCTGAGGGGCTAAA		158
135-85/20D6 / 86-4	GATGTTCAACCTATGAAGAA [G/C] AACACCCGAGGACCAACGAG		159
136-85/20D6 / 86-5	CCATTAGTGAAGGGAGGCATGT [T/A] CCTGTCACACATTGATGATG		160

137-85/20D6/86-8	AAACACATGCCAAAGATCC [CG/AA] ACACTCGAGAAAGAGTGGAG	161
138-N1/20D8/N2	CTCATAGGGATCTGGAGTA [T/G] GCAAATCGAATCTCCTCTCC	162
139-N1/20E1/N2	TGCACGCCCTCACCTGTTCTCT [T/A] CCAATCTGACATCAAGGATT	163
140-N1/20F1/N2-1	NGTGTGTTTGAGGTGAAAGC [A/T] ACAAAATGGAGATAACCTTTT	164
141-N1/BoC-a2/N3-2	CCCGAGCCATTAGGACAAGA [T/C] GACTTGCCGTTGACCAAAC	165
142-N1/BOC-A2/N3-1	CCCATCTCATCCTTCTTGA [A/G] CCGTTGAATCAAGCTCCTGG	166
143-N1/BoC-a2/N3-3	TACATTCATATTGGTTGGTT [C/A] TTGGGAAATAAAGTACCAAC	167
144-86/SC3	GCACGGGCTAGAGTTGTTGC [C] AGAAGGAATGAAACATCTGA	168
145-N3/SC3/N4-1	CTTGAGAACCTATAGTCCTGT [A/T] GTTCCGGTCCGCCACAGTTCG	169
146-N3/SC3/N5-1	CACAGTTGGTACAGTTCTTC [A/C] CATTGCCACTGTTATGCCACT	170
147-N1/SC3/N3-1	GAAGGGGTCCACTATCTTGA [A/G] ACCTATAAGTCCTGGTTTCG	171
148-86/SC3/N4-1	TCCCGGAAATCTTGCTGAAA [A/C] CGTTTACCTGGACAAACCAG	172
149-B11/N5-1	ATGGTCTTCAAAAGTGTCTGT [T] GCAACGGCACGTCCGAACAAG	173

Please insert the accompanying paper copy of the sequence listing, page numbers 1-37, before the claims.

REMARKS

The information contained in the computer readable form of Application No. 08/813,507 was prepared through the use of the software program "PatentIn" and was identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the claims by the amendment. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



Joe Liebeschuetz
Reg. No. 37,505

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
Tel: (650) 326-2420
Fax: (650) 326-2422
JOL:adm
PA 3193060 v1

VERSION WITH MARKINGS TO SHOW CHANGES MADE

The paragraph beginning on page 4, line 9 has been amended as follows:

Fig. 1 shows probe array tiles (SEQ ID NOS:3-29) for two allelic forms of the [Brassira] Brassica 18A2 polymorphism (SEQ ID NOS:1 and 2).

Table 1 beginning on page 8, line 10 has been amended as follows:

TABLE 1

Marker Name	Sequence	SEQ ID NO
1-85/5B5/86-1	AGCAAGCTTACATGCGTGGAA [GT/AA] GAGAGTCCCGAGATCAACC	<u>30</u>
2-85/5B12/N3-1	CCTTGATCTCTCAAGTAATC [A/G] TCTCACCGGAAGATCCCTGA	<u>31</u>
3-85/5C3/86-2	ACCATCCATTAAACTGTATC [A/G] TCGCAATCTAACCAAAAGTT	<u>32</u>
4-85/5E1/86-1	TAAAGCAAAGAGAGTCTTAC [C/A] GTCTGCTGCATGATAACCC	<u>33</u>
5-85/5E1/86-2	CTACTGATAAGTGAAACCACCC [A/C] ATCCCCAAATTAAAGCAA	<u>34</u>
6-85/6A11/86	ATCCTATTGGTAGTAACACA [G/A] ATTGAGTTAACATGTTGCAGGG	<u>35</u>
7-N1/6A11/N2	AGGCAAAGGGTAGTTGCAA [G/A] ACTGCCTCTCACCGAGGTAAT	<u>36</u>
8-N1/6A9/N2-1	CCAGCTTCAATGTCATG [C/A] TTGTGTCATGCCAAAGTTC	<u>37</u>
9-N1/6A9/N2-2	AAAGTTCATTACGATGATCT [A/G] ACCCTGCAGTCATCCATGGA	<u>38</u>
10-85/6A12/86	CTTCCCCCCCCTCAATACCTC [T/G] TTCAAAAGTGAAGTGCAG	<u>39</u>
11-N1/6D1/N2-1	ATTTTTGTTTTGTTCTGTTC [G/C] GGTCAAGGTCAAGAACAAAGTT	<u>40</u>
12-N1/6H5/N2	AAACCAGGCCACCTCCCTTA [C/] CCACCTCATCGTTCCCTTC	<u>41</u>
13-86/6F11/N2-2	GATTTCGACCGCAGTCTCAC [G/T] GAGGTGAGTATATCGCTTT	<u>42</u>
14-N1/6F11/N2	TAGGACAGGCCAAACAAATCTA [C/A] GCGGTCAAATCCGATTTCG	<u>43</u>
16-N1/8B5/N2	ACTCAAAAAAACGATAACCTC [G/C] GCCGTCTCTGCCGTCTCGC	<u>44</u>
17-N1/8D4/N2-1	CAGGAGACAGTTACAGTCCC [A] CAGAGTCGCCAGGATCTCGAA	<u>45</u>
18-85/8D4/86-2	CTGATCTTGAAGGAGAGACC [A/G] CCACAAGGTTCCATCCTATG	<u>46</u>
19-85/8H11/86	AGTGCAGGGCTCAGTTGGAT [G/T] ATTAGGGTGTCAAGTAAATCA	<u>47</u>
20-85/10B8/86	NAGGTCCATGATGACAA [T/A] AAAGGTATTCCACATGTCAA	<u>48</u>
21-N2/10B8/N3-2	ACATCCAAACTTCTCCAGT [T/C] CTTTATCCCTGATTG	<u>49</u>

21-N2/10B8/N3-2	ACATCCAACCTTTCTCCAGT [T/C] CTTTATTCTATCCCTGATTTG	50
22-N2/10B8/N3-1	AAGGTATTCCATGGTATAC [A/C] TCCAACCTTTCTCCAGTTCT	<u>51</u>
23-85/10B9/86	GACTTCTGGAAAGAAAG [T/C] TGTAACCGCGTGTGAGATTCTG	<u>52</u>
24-10C8/N2	ATAGAAACCGCCGATGGTCA [A] GGACACGCCAACCGTCCTTCGT	<u>53</u>
25-10C8/N2	CACTTTCTCGTGGCTAAAT [T] CTTCGGGCGAGCCGGTCTCA	<u>54</u>
26-10D2/N1	GTTATCATCAGTACCGGTAT [T] AACCCAAAGGCTAATTCTTA	<u>55</u>
27-85/10D2	TTGGGTATCTACGGACTGAT [C] ATGGCTGTTATCATCAGTAC	<u>56</u>
28-N1/10E12/N2-1	GGAATTCAAACTTCGCCAAC [G/T] TCTTCATTGCTGTCGGC	<u>57</u>
29-N1/10E12/N2-2	TCCCTTACGGCTTCAAGCGCA [C/G] CGGCTGGCTCATGGGTGTCC	<u>58</u>
30-N1/10F4/N2	TGTATCTATGCGGTTGGCTGC [G/C] GTCTCCGGTCGCCAGTAC	<u>59</u>
31-10F4/N2	GGCCAGTAGTACGCCGGTTAC [A] ATCTCACTGCCTTCACGTCC	<u>60</u>
32-85/10F4/N2	GGCCAGTAGTACGCCGGTTAC [G/A] ATCTTAATGCCTTCACGTTC	<u>61</u>
33-85/10F9/N1-2	AACTTGAATTCCACAACTT [G/C] AGAAACCTTCGATGTGGTGCC	<u>62</u>
34-85/10F9/86	CGGTACTCGGAAAGCTGGAG [C/G] ATCAAACTTGGAATTCCACAA	<u>63</u>
35-86/10F12	AAAAGTGCATTGTTCAAGGT [G] GATGCTGCTCCGGTCAAGCA	<u>64</u>
36-85/10H6/86	GTCAAAAGCCACGGATTCAA [G/A] AACGTGCTCTTGGCCT	<u>65</u>
38-85/10F12/86	AAACCGGGTCCATTGATGTG [T] GTCTACAAAGCTTCAAACAA	<u>66</u>
39-85/11B7/86	ANACCCCTGAGCTCATGGCT [C/T] TGACCCATGTTCTTGCACC	<u>67</u>
40-85/11C4/86	TTGGGACCGTTGGAGTTGC [A/G] TCTGGCTATGACGGTGGGA	<u>68</u>
41-85/11D4/86-2	AACTTTGCCATTGCTGTCA [A/G] TATCTTCGTCAAGCTTCAGCT	<u>69</u>
43-N2/11D11/N3	GACAACGGCTGGTGGTATTGCG [C/T] GAAATGGCTGGATGAGCCA	<u>70</u>
44-86/11D11/N3	GCTGCTCTAGGGATGCTAG [C/T] ACCATGCCACCGGGTTGGC	<u>71</u>

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45-85/11D11/86	ATGCTCAGCACCATGCCAC [T/C] GGTTTGGCGATTGATGCTTA	72
46-N2/11E3/N8a	GAGAAAGTGTGGAGAT [C/T] TACAaGTCCATACTGATGGCC	<u>73</u>
47-86/11E3/N2a	AATGCTTGTGGAGATTACA [G/A] GTCCATACTGATGGCGAGG	<u>74</u>
48-86/11E3/N2b	AATGCTTGTGGAGATCTACA [G/A] GTCCATACTGATGGCGAGG	<u>75</u>
49-85/11F12/86	AATGATTGGTTGAGAAGCA [T/A] ACAGCTGGTACGCTTGATAT	<u>76</u>
50-85/11F7/86	GATAGGGCGAAGAGAGGGAA [G/A] AGTCCCTGAGAGGAAAGAGAT	<u>77</u>
51-85/11H2/86-2	CTCTCTCTCCACAAAGACAC [A/C] GCTTTCTCCATGACCTTCCGG	<u>78</u>
52-85/11H5/86-2	TCTCTGACGTCATGAAAGCT [C/A] ATGGCAAAATGCTGATGCA	<u>79</u>
53-85/11H6/86-1a	GTATCGATCGGTTGGTCCG [T/C] GAAACCCAAAATCACCTTT	<u>80</u>
54-85/11H6/86-1b	GTTATCGATCGGTTGGTCCG [T/C] GAAACCCAAAATCACCTTT	<u>81</u>
55-85/12B6/N3	CGTCAGCC"TTCTCGGCCGC [A/C] GTCGTCCCTCGAACCGTGC	<u>82</u>
56-86/12B6/85a	TGTCCTTCCGTCAGCCCTTC [C/T] TCCGCCCGTGTCCCTCCG	<u>83</u>
57-86/12B6/85b	TGTCCTTCCGTCAGCCCTTC [C/T] TCCGCCCGTGTCCCTCCG	<u>84</u>
58-86/12B11/85	TCAAGGTTAACCTCTATATAT [T/] ATATTTCATGGTATGAAGGT	<u>85</u>
59-n1/12B11/N2-2	TATCCTGCAAATGACATT [T/C] CCTTCAGGTTCTAGAAGCTG	<u>86</u>
60-85/12C2/86	CGAGAACAGAAAGAGAGA [C/] TGGAACACGTGGACAGTAC	<u>87</u>
62-12C11/N2	ACGGGTCC"TAGGGCCATGGC [T] ATTTCCTCACCGTTCTGG	<u>88</u>
63-N1/12D10	TTGGGCTTTCGGTGGTATGA [T] CTTCGTCCCTCGTCTATTGCA	<u>89</u>
65-85/12F4/86-1	TCCTTGATTCCTTAATAATC [A/T] TTGGCTGGGGTCTTCTAA	<u>90</u>
66-12G5/N1	GCTTGAATAACGATGTCTAC [T] CTGCCTCGGCGTACGGGGGA	<u>91</u>
67-85/12G8	CTAAAAGATCGGACGAGTGT [C] CCTTACTACGCTCCCATCTAT	<u>92</u>

68 - 12G9/N1 - 1	AGGTGGTTAGCGTGGCAT [C] CGATCCATTGGATCCA	93
69 - 85/12G9 /	NGTGGTTACCGTATCATT [T] GATCCATTGGATGGATCGAG	<u>94</u>
70 - 12B11/N2 - 1	GCGGATCCTATATTGGTCT [T] GATGGATTGTTCTATCCCG	<u>95</u>
71 - /12B11/N2 - 2	TATCCTGCAAATTGACATT [C] CCTTCAGGTTCTAGAAGCTG	<u>96</u>
72 - N1/12E10	TACCA CGGTCTGTA CTTGGTCA [A] TGTCTGGAA CGTCACCAAGC	<u>97</u>
73 - N1/13A3/N2a	CTGTCTCAGTTGTGGATC [C/G] AAATCGAAATCGAAAGCGTAC	<u>98</u>
74 - N1/13A3/N2b	CTGTCTCAGTTGTGGATC [C/G] AAATCAAAATCGAAAGCGTAC	<u>99</u>
75 - 13E8/N2	ACACTGTTGGAGGA CGTGAA [G] AAGATATTCAAGACAAACATC	<u>100</u>
76 - N1/13F6/N2 - 2	TCTTTCTGTATCTTGTGAGT [C/T] GTTACGCCTGTCAACACCCG	<u>101</u>
77 - 13F8/N2 - 1	GGAACCCCTAGGGAGCCACA [G] CTCCTTATGCTTAAGGGCGT	<u>102</u>
78 - 13F8/N2	GATCATAAGTATCCGCCGGAA [C] CCTAGGGAGCCCACAGCTCC	<u>103</u>
79 - 85/14B5/86	TTCGGGGGGTGCGATCCGGGC [A/G] GAAGACATTTGTCAGGTGANN	<u>104</u>
80 - N1/14C2/N2	GCACCAACATTGTAAACCTA [T/G] AGCTTCTCAGCCACCT	<u>105</u>
81 - 85/14C2/86 - 1	GCTGCCACATAGTGAACCTA [T/A] AGCTTCTCAGCCACCT	<u>106</u>
82 - N2/14C2/85 - 2	GCACCAACATTGTGAACCTA [G/A] AGCTTCTCAGCCACCT	<u>107</u>
83 - 85/14C2/86 - 2	AGTACATAGCTATTGACTAA [C/G] TTAAGTTCTTGTATTGTTG	<u>108</u>
84 - N2/14C2/85 - 1	CCTCTATCGCCATGGTTGC [A/T] CAAACATTTGTGAAACCTAGAG	<u>109</u>
85 - 85/14E2/86 - 2	TTGACCCCTGGCAAGGCCACC [G/T] GTCAAGGCCATGCTGCAGCCT	<u>110</u>
86 - 85/14E2/86 - 1	AGGCTGCCCTCTCCAATTCA [A/C] AAAGCCA ACTCCTAAACCAA	<u>111</u>
87 - 85/14E8/86	AAACATGGAAAGGCCGTGATA [/ G] TCACCCGGTCAAGGCTCACCGTC	<u>112</u>
88 - 85/14E12/86	CAACCTGAAAATTGTTTA [C/A] CAACGGCCCCGTTCTCCA	<u>113</u>

89-14H10/86	AAGGCCAACGACATTAC [C] TCCATCGTTAGCAAACGGAGG	<u>114</u>
90-85/14H10/86	TCACCGGGCTTGAAGTCTTCC [G/T] CTGCATTCCCAGTCACCCGC	<u>115</u>
91-85/15A6/86	ACTCAGCTTCTTATGCCTC [G/] ACTTGCGACACAGGAATCCA	<u>116</u>
92-85/15C4/86	TGGGCTAACATCTGGTG [G/T] TCACCTTAACCCAGGCCGTAN	<u>117</u>
93-85/15E5/86-1	CGAGGATCACTTCTCTGT [G/T] CAAGAAGAAGTTCGGCAAGG	<u>118</u>
94-N1/15E5/N2-1	CTGTTCAAGAAGGTTCGG [C/T] AAGGTCTACGCTTCCCGGA	<u>119</u>
95-N1/15E5/N2-2	CCCTCTGCTCGTCACGGGCTAC [A/T] GATTCTCCGGATCTGAC	<u>120</u>
96-86/15E5/N2	CCCGCAGGAGGACGACTAC [A/T] CGCGCAGTTCTAAATCC	<u>121</u>
97-15E9/86	TCCACTGCCGGAAAGAAC [T] CGACAAACCGGTTGTCTACTT	<u>122</u>
98-N2/15E9	ATGGCTCGGACGGGTCTCC [G] GTAAACCTCGGAGGAGAT	<u>123</u>
99-N2/15E9/86	GCCGACTCTCGAAAGTTCTT [A/] ACTCCACTCGCCGGAAAGAA	<u>124</u>
100-85/15E9/86-1	GAATCTAGGAGAGCAGATCT [T/G] CCTCTCTATCTCAATGTTCT	<u>125</u>
101-85/15E9/86-2	TCCACTGCCGGAAAGAAC [C/T] CGACAAACCGGTTGTCTACAT	<u>126</u>
102-N1/15E9/N2-1	GTCATGAAGATATTCACTAC [A/G] CGGACTCTCGAAGCTTCTTA	<u>127</u>
103-85/15F1/86	GCAGGGTAAAAATTCTACAGAC [C/A] TTCCCTTTCAATTGTAGTTA	<u>128</u>
105-85/15F10/86	GTGCCCTAAAGATAACCCCTCA [A/G] GCTTGGTGTCTGGGCTAATG	<u>129</u>
106-N2/15G1	TTCTTCCCACAGGTAAACT [T] GCTAAACTTCTTCCAAAGTA	<u>130</u>
107-N1/15H7/N2	TATGTATCAGGACAATGTGT [GA/TT] GTGACTGTGGTGCATCCAT	<u>131</u>
108-N1/16A1/N2-1	GCTAAGCTACGCCAACTGCCA [C/T] CAATCAGGGCAAGCTAAAGG	<u>132</u>
109-85/16A5/86	TATACACTCTTTAAAGGGT [G/C] TGTGTGTACCCATCTCTCTT	<u>133</u>

110 -N1/16B6/N2	ATGGCTGGGTATTGGCTGTC [C/T] AAGGCTGGATCTTGGTCCCA	<u>134</u>
111 -85/16B6/N1	GGATCCATCTCAACTATGGT [A/C] GTATTATCGTTGAGGCTAGG	<u>135</u>
112 -85/16B7/86	GTATGTGATTGGAAAGAGAA [T/T] CAAACTAAGTGCCGAGAAAG	<u>136</u>
113 -N1/16D6/N2	GCTAAGGTAGTTGGAGGC [CAA/GTG] CCACAGCCACGGGACTAAGG	<u>137</u>
114 -85/16D10/86	CTCAACCGTAGCAAGTAATAA [T/G] ATACTGTCTATTATGGTTA	<u>138</u>
115 -N1/16E9/N2	AGACTTTCCCCATTCTCTTC [T/A] CCATCCACCGTGGAAACCCA	<u>139</u>
116 -85/16H3/86 -1	ACTTCGAAAACTGTAAACCTA [A/T] ACTTTAACAGAGTTAGAGCTA	<u>140</u>
117 -85/16H3/86 -2	CACCATCGAGAAAGGGTA [C/T] TTGAAACCTGTAAACCTAAA	<u>141</u>
118 -85/17A5/86	CTAAGGGGTCTCTGAAGAA [A/G] TACAGAGAGTCGAAGAGAT	<u>142</u>
119 -85/17C7/86	CCGGGGACGACGCCCTTCTTC [C/A] TCTGCTCCACCGCGAGGCC	<u>143</u>
120 -85/17F7/86	GAGGAGTAGTCTCCATGGCC [G/] AAGAAGAGCGTCCGGAGACCTG	<u>144</u>
121 -85/17G12/86	GAAAGTTAGGGCTTCTAACAT [C/T] AGTTTGGCAAGGCTTTAAC	<u>145</u>
122 -85/18A2/86	TCAAAACTAATATTCTTTT [G/C] TTGATTGGTAATAAACAGGT	<u>146</u>
123 -85/18A11/86	TTCCAGTGAAAAGGCATTGT [T/G] CTCCAAAATCTCGCTCTGCG	<u>147</u>
124 -85/18F5/86	AAGCAGCTCTGACTGAATG [C/A] GAGAGGTAAATCAGACTGTG	<u>148</u>
125 -85/18H10/86 -3	TAGATTGAAGCAATCAAGAA [G/A] ATCTCAGACTTCATCACCCA	<u>149</u>
126 -85/19B3/86	GCATCCAAACTCCAAAGGATGA [/C] CCTGCCAAGGTGCTGCTAACT	<u>150</u>
127 -85/19C8/86	GAGCTCAGGGATGGGATC [A/T] GACTACCTTGGAAAGGGTGT	<u>151</u>
128 -N1/19F4/N2	TGGGGTTAGTCGAAATAGGT [A/T] AAATGCTTGTGTTGTA	<u>152</u>
129 -N1/19H1/N2	TACGGCGAGCAGGACTTGG [G/A] ACGCAAGCAATGAGCTTTT	<u>153</u>
130 -85/20B4/86 -1	GAAGCCCATTGGTACGGAGGCC [G/A] GAGAGAGTCAGTACTTGGG	<u>154</u>

131 -N1/20B12/N2	AACGGGTCACTGCTAAATCA [T/A] AAGGATCACAAAGGCTGGGAC	155
132 -85/20C12/86	CTAGCCTACTTTGGAAAAAG [T/T] TTGGTTATTGGTTGTGTGG	<u>156</u>
133 -85/20D2/86	GACTTCAAGGACTTCGCCGG [A/C] AAATGCTCCGACCGCTGTCAA	<u>157</u>
134 -85/20D3/86-2	GAGGAGGGCTACATGCAGCT [G/A] AAGAGGCTGAGGGGGCTAAA	<u>158</u>
135 -85/20D6/86-4	GATGTTCAACCTATGAAGAAA [G/C] AAACACCCGAGGACCAACGAG	<u>159</u>
136 -85/20D6/86-5	CCATTAGTGAGGGAGCATGT [T/A] CCTGTCACATTGATGATGT	<u>160</u>
137 -85/20D6/86-8	AAACACATGCCAAAGATCC [CG/AA] ACACCTGAGAAAGAGTGGAG	<u>161</u>
138 -N1/20D8/N2	CTCATAGGGGATCTGGAGTA [T/G] GCAAATCGAAATCTCCTCTCC	<u>162</u>
139 -N1/20E1/N2	TGCACGGCTCACTTGTTCT [T/A] CCAATCTGACATCAAGGATT	<u>163</u>
140 -N1/20F1/N2-1	NGTGT'TTTGAGGTGAAAGC [A/T] ACAAAATGGAGATAACCTTTT	<u>164</u>
141 -N1/BoC-a2/N3-2	CCCGAGCCATTAGGACAAGA [T/C] GACTTGCCTTGACCAAAC	<u>165</u>
142 -N1/BOC-A2/N3-1	CCCATCTCATCCCTTCTTGAA [A/G] CGCTTGAAATCAAGCTCCTGG	<u>166</u>
143 -N1/BoC-a2/N3-3	TACATTCTCATGGTTGGTT [C/A] TTGGAAATAAAGTACCAAC	<u>167</u>
144 -86/SC3	GCACGGCTAGAGTGTGTC [C] AGAAGGAATGAACAAATCTGA	<u>168</u>
145 -N3/SC3/N4-1	CTTGAGACCTATAGTCCTGT [A/T] GTTGGTTCCGCCACAGTTCG	<u>169</u>
146 -N3/SC3/N5-1	CACAGTTCGTACAGTTCTTC [A/C] CATTGCCACTGTATGCAC	<u>170</u>
147 -N1/SC3/N3-1	GAAGGGCGTCCACTATCTTGA [A/G] ACCTATAGTGTGTTTCG	<u>171</u>
148 -86/SC3/N4-1	TCCCGGAAATCTTGTGAA [A/C] CGTTTACCTGCGACAAACCAG	<u>172</u>
149 -B11/N5-1	ATGTCTCAAAGTGTCTGT [T] GCAAACGGCACGTCCGAAACAAG	<u>173</u>